

Table 2. MCSs with evidence of a conserved RNA secondary structure.

MCS Position ^a	Log-odds ^b	Approximate Locations
183738-184135	10.9	100 kb downstream of <i>TES</i>
354345-354641	18.7	<i>CAV1</i> 5' UTR
367787-367893	4.3	9 kb downstream of <i>CAV1</i> exon 3
389745-389958	4.8	<i>CAV1</i> 3' UTR
390345-390721	5.3	<i>CAV1</i> 3' UTR
501536-501684	7.3	250 bp upstream of <i>MET</i>
527917-528302	13.1	260 bp upstream <i>MET</i> exon 2
692015-692207	23.4	upstream and 5' UTR of <i>CAPZA2</i>
692352-692463	13.7	170 bp downstream of <i>CAPZA2</i> exon 1
747889-748392	3.1	450 bp downstream of <i>CAPZA2</i> 3' UTR
748416-748501	0.03	1 kb downstream of <i>CAPZA2</i> 3' UTR
782972-783041	13.6	<i>ST7</i> 5' UTR
783054-783341	22.2	<i>ST7</i> exon 1
849613-849605	11.3	67 kb downstream of <i>ST7</i> exon 1
850761-850802	4.6	67 kb downstream of <i>ST7</i> exon 1
855569-855698 (A)	47.6	72 kb downstream of <i>ST7</i> exon 1
961398-961517	5.9	<i>ST7</i> exon 6
967021-967347	11.3	1.2 kb downstream of <i>ST7</i> exon 7
987204-987314	1.8	14 kb upstream of <i>ST7</i> exon 9
1002543-1002951	1.1	2.5 kb downstream of <i>ST7</i> exon 9
1018825-1018945	11.3	<i>ST7</i> exon 10
1019574-1019879 (B)	26.3	700 bp downstream of <i>ST7</i> exon 11
1150088-1150388	25.6	<i>WNT2</i> exon 4
1152428-1152700	33.9	<i>WNT2</i> 5' UTR
1153944-1154196	48.3	800 bp upstream of <i>WNT2</i> 5' UTR
1154720-1154797	6.1	1.8 kb upstream of <i>WNT2</i> 5' UTR
1497719-1497883	0.18	<i>CFTR</i> 3' UTR
1541121-1541326	7.5	<i>CORTBP2</i> exon 21
1613775-1614079	6.9	<i>CORTBP2</i> intron 4 and exon 5

^aCoordinates within the human reference sequence of the targeted region, as displayed in the customized UCSC Genome Browser (see <http://genome.ucsc.edu>). The predicted RNA secondary structures of the MCSs marked with (A) and (B) are displayed in Figure 5A and 5B, respectively.

^bMeasure of how much better the MCS fits a model for an RNA secondary structure as opposed to one for coding or non-functional sequence (see text and Methods).